

1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/687,230A

DATE: 07/11/2002
TIME: 13:27:28

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Output Set: N:\CRF3\07112002\I687230A.raw

ENTERED

3 <110> APPLICANT: Braselmann, Sylvia
5 <120> TITLE OF INVENTION: Nucleotide Sequences that Encode Phosphatidylinositol-3'
Kinase

6 Associated Proteins and Uses Thereof
8 <130> FILE REFERENCE: ONYX1027-DIV1
10 <140> CURRENT APPLICATION NUMBER: US 09/687,230A
11 <141> CURRENT FILING DATE: 2000-10-13
13 <150> PRIOR APPLICATION NUMBER: US 08/942,008
14 <151> PRIOR FILING DATE: 1997-10-01
16 <150> PRIOR APPLICATION NUMBER: US 60/030,103
17 <151> PRIOR FILING DATE: 1996-11-01
19 <160> NUMBER OF SEQ ID NOS: 3
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2307
25 <212> TYPE: DNA
26 <213> ORGANISM: Phosphatidylinositol-3' Kinase
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (162)..(1928)
31 <223> OTHER INFORMATION:
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37 gcggggcccg ctcccgccct ccgctcgccct ggcccgacc ggaagcggc ccgcacggcc 120
39 tgggcctggc gcggggggcg ggcaccgggg ccggtcgga c atg ggc aag aag cac 176
40 Met Gly Lys Lys His
41 1 5
43 aag aag cac aag tcg gac aaa cac ctc tac gag gag tat gta gag aag 224
44 Lys Lys His Lys Ser Asp Lys His Leu Tyr Glu Glu Tyr Val Glu Lys
45 10 15 20
47 ccc ttg aag ctg gtc ctc aaa gta gga ggg aac gaa gtc acc gaa ctc 272
48 Pro Leu Lys Leu Val Leu Lys Val Gly Gly Asn Glu Val Thr Glu Leu
49 25 30 35
51 tcc acg ggc agc tcg ggg cac gac tcc agc ctc ttc gaa gac aaa aac 320
52 Ser Thr Gly Ser Ser Gly His Asp Ser Ser Leu Phe Glu Asp Lys Asn
53 40 45 50
55 gat cat gac aaa cac aag gac aga aag cgg aaa aag aga aag aaa gga 368
56 Asp His Asp Lys His Lys Asp Arg Lys Arg Lys Lys Arg Lys Lys Gly
57 55 60 65
59 gag aag cag att cca ggg gaa gaa aag ggg aga aaa cgg aga aga gtt 416
60 Glu Lys Gln Ile Pro Gly Glu Glu Lys Gly Arg Lys Arg Arg Arg Val
61 70 75 80 85
63 aag gag gat aaa aag aag cga gat cga gac cgg gtg gag aat gag gca 464
64 Lys Glu Asp Lys Lys Lys Arg Asp Arg Asp Arg Val Glu Asn Glu Ala

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65	90	95	100	
67 gaa aaa gat ctc cag tgt cac gcc cct gtg aga tta gac ttg cct cct				512
68 Glu Lys Asp Leu Gln Cys His Ala Pro Val Arg Leu Asp Leu Pro Pro				
69	105	110	115	
71 gag aag cct ctc aca agc tct tta gcc aaa caa gaa gaa gta gaa cag				560
72 Glu Lys Pro Leu Thr Ser Ser Leu Ala Lys Gln Glu Glu Val Glu Gln				
73	120	125	130	
75 aca ccc ctt caa gaa gct ttg aat caa ctg atg aga caa ttg cag aga				608
76 Thr Pro Leu Gln Glu Ala Leu Asn Gln Leu Met Arg Gln Leu Gln Arg				
77	135	140	145	
79 aaa gat cca agt gct ttc ttt tca ttt cct gtg act gat ttt att gct				656
80 Lys Asp Pro Ser Ala Phe Phe Ser Phe Pro Val Thr Asp Phe Ile Ala				
81 150	155	160	165	
83 cct ggc tac tcc atg atc att aaa cac cca atg gat ttt agt acc atg				704
84 Pro Gly Tyr Ser Met Ile Ile Lys His Pro Met Asp Phe Ser Thr Met				
85	170	175	180	
87 aaa gaa aag atc aag aac aat gac tat cag tcc ata gaagaa cta aag				752
88 Lys Glu Lys Ile Lys Asn Asn Asp Tyr Gln Ser Ile Glu Glu Leu Lys				
89	185	190	195	
91 gat aac ttc aaa cta atg tgt act aat gcc atg att tac aat aaa cca				800
92 Asp Asn Phe Lys Leu Met Cys Thr Asn Ala Met Ile Tyr Asn Lys Pro				
93	200	205	210	
95 gag acc att tat tat aaa gct gca aag aag ctg ttg cac tca gga atg				848
96 Glu Thr Ile Tyr Tyr Lys Ala Ala Lys Lys Leu Leu His Ser Gly Met				
97	215	220	225	
99 aaa att ctt agc cag gaa aga att cag agc ctg aag cag agc ata gac				896
100 Lys Ile Leu Ser Gln Glu Arg Ile Gln Ser Leu Lys Gln Ser Ile Asp				
101 230	235	240	245	
103 ttc atg gct gac ttg cag aaa act cga aag cag aaa gat gga aca gac				944
104 Phe Met Ala Asp Leu Gln Lys Thr Arg Lys Gln Lys Asp Gly Thr Asp				
105	250	255	260	
107 acc tca cag agt ggg gag gac gga ggc tgc tgg cag aga gag aga gag				992
108 Thr Ser Gln Ser Gly Glu Asp Gly Gly Cys Trp Gln Arg Glu Arg Glu				
109	265	270	275	
111 gac tct gga gat gcc gaa gca cac gcc ttc aag agt ccc agc aaa gaa				1040
112 Asp Ser Gly Asp Ala Glu Ala His Ala Phe Lys Ser Pro Ser Lys Glu				
113	280	285	290	
115 aat aaa aag aaa gac aaa gat atg ctt gaa gat aag ttt aaa agc aat				1088
116 Asn Lys Lys Lys Asp Lys Asp Met Leu Glu Asp Lys Phe Lys Ser Asn				
117	295	300	305	
119 aat tta gag aga gag cag gag cag ctt gac cgc atc gtg aag gaa tct				1136
120 Asn Leu Glu Arg Glu Gln Glu Gln Leu Asp Arg Ile Val Lys Glu Ser				
121 310	315	320	325	
123 gga gga aag ctg acc agg cgg ctt gtg aac agt cag tgc gaa ttt gaa				1184
124 Gly Gly Lys Leu Thr Arg Arg Leu Val Asn Ser Gln Cys Glu Phe Glu				
125	330	335	340	
127 aga aga aaa cca gat gga aca acg acg ttg gga ctt ctc cat cct gtg				1232
128 Arg Arg Lys Pro Asp Gly Thr Thr Thr Leu Gly Leu Leu His Pro Val				
129	345	350	355	

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131 gat ccc att gta gga gag cca ggc tac tgc ctg gtg aga ctg gga atg      1280
132 Asp Pro Ile Val Gly Glu Pro Gly Tyr Cys Leu Val Arg Leu Gly Met
133      360      365      370
135 aca act gga aga ctt cag tct gga gtg aat act ttg cag ggg ttc aaa      1328
136 Thr Thr Gly Arg Leu Gln Ser Gly Val Asn Thr Leu Gln Gly Phe Lys
137      375      380      385
139 gag gat aaa agg aac aaa gtc act cca gtg tta tat ttg aat tat ggg      1376
140 Glu Asp Lys Arg Asn Lys Val Thr Pro Val Leu Tyr Leu Asn Tyr Gly
141 390      395      400      405
143 ccc tac agt tct tat gca ccg cat tat gac tcc aca ttt gca aat atc      1424
144 Pro Tyr Ser Ser Tyr Ala Pro His Tyr Asp Ser Thr Phe Ala Asn Ile
145      410      415      420
147 agc aag gat gat tct gat tta atc tat tca acc tat ggg gaa gac tct      1472
148 Ser Lys Asp Asp Ser Asp Leu Ile Tyr Ser Thr Tyr Gly Glu Asp Ser
149      425      430      435
151 gat ctt cca agt gat ttc agc atc cat gag ttt ttg gcc acg tgc caa      1520
152 Asp Leu Pro Ser Asp Phe Ser Ile His Glu Phe Leu Ala Thr Cys Gln
153      440      445      450
155 gat tat ccg tat gtc atg gca gat agt tta ctg gat gtt tta aca aaa      1568
156 Asp Tyr Pro Tyr Val Met Ala Asp Ser Leu Leu Asp Val Leu Thr Lys
157      455      460      465
159 gga ggg cat tcc agg acc cta caa gag atg gag atg tca ttg cct gaa      1616
160 Gly Gly His Ser Arg Thr Leu Gln Glu Met Glu Met Ser Leu Pro Glu
161 470      475      480      485
163 gat gaa ggc cat act agg aca ctt gac aca gga aaa gaa atg gag cag      1664
164 Asp Glu Gly His Thr Arg Thr Leu Asp Thr Gly Lys Glu Met Glu Gln
165      490      495      500
167 att aca gaa gta gag cca cca ggg cgt ttg gac tcc agt act caa gac      1712
168 Ile Thr Glu Val Glu Pro Pro Gly Arg Leu Asp Ser Ser Thr Gln Asp
169      505      510      515
171 agg ctc ata gcg ctg aaa gca gta aca aat ttt ggc gtt cca gtt gaa      1760
172 Arg Leu Ile Ala Leu Lys Ala Val Thr Asn Phe Gly Val Pro Val Glu
173      520      525      530
175 gtt ttt gac tct gaa gaa gct gaa ata ttc cag aag aaa ctt gat gag      1808
176 Val Phe Asp Ser Glu Glu Ala Glu Ile Phe Gln Lys Lys Leu Asp Glu
177      535      540      545
179 acc acc aga ttg ctc agg gaa ctc cag gaa gcc cag aat gaa cgt ttg      1856
180 Thr Thr Arg Leu Leu Arg Glu Leu Gln Glu Ala Gln Asn Glu Arg Leu
181 550      555      560      565
183 agc acc aga ccc cct ggg aac atg atc tgt ctc ttg ggt ccc tca tca      1904
184 Ser Thr Arg Pro Pro Gly Asn Met Ile Cys Leu Leu Gly Pro Ser Ser
185      570      575      580
187 gag aaa tgc atc ttg ctg aac aag tgaccaataa tcttaaagaa ttgcacagca      1958
188 Glu Lys Cys Ile Leu Leu Asn Lys
189      585
191 agtaactoca ggtgatatcg taagcacgta tggagttcga aaagcaatgg ggatttccat      2018
193 tccttcccccc gtcattgaaa acaactttgt ggatttgaca gaagacactg aagaacctaa      2078
195 aaagacggat gttgatgagt gtcgacctgg tggaagttag ggctgcctgg tatttgatta      2138
197 tatattatgt acatactttt tcattcttaa cttagaaatg cttttcagaa gatattaaat      2198

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199 atttgtaaatt tgtgttttta attaaacttt tggaacagcg aatttggatg ttccagaggt 2258
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206 <212> TYPE: PRT
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209 <400> SEQUENCE: 2
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212 1 5 10 15
215 Glu Tyr Val Glu Lys Pro Leu Lys Leu Val Leu Lys Val Gly Gly Asn
216 20 25 30
219 Glu Val Thr Glu Leu Ser Thr Gly Ser Ser Gly His Asp Ser Ser Leu
220 35 40 45
223 Phe Glu Asp Lys Asn Asp His Asp Lys His Lys Asp Arg Lys Arg Lys
224 50 55 60
227 Lys Arg Lys Lys Gly Glu Lys Gln Ile Pro Gly Glu Glu Lys Gly Arg
228 65 70 75 80
231 Lys Arg Arg Arg Val Lys Glu Asp Lys Lys Arg Asp Arg Asp Arg
232 85 90 95
235 Val Glu Asn Glu Ala Glu Lys Asp Leu Gln Cys His Ala Pro Val Arg
236 100 105 110
239 Leu Asp Leu Pro Pro Glu Lys Pro Leu Thr Ser Ser Leu Ala Lys Gln
240 115 120 125
243 Glu Glu Val Glu Gln Thr Pro Leu Gln Glu Ala Leu Asn Gln Leu Met
244 130 135 140
247 Arg Gln Leu Gln Arg Lys Asp Pro Ser Ala Phe Phe Ser Phe Pro Val
248 145 150 155 160
251 Thr Asp Phe Ile Ala Pro Gly Tyr Ser Met Ile Ile Lys His Pro Met
252 165 170 175
255 Asp Phe Ser Thr Met Lys Glu Lys Ile Lys Asn Asn Asp Tyr Gln Ser
256 180 185 190
259 Ile Glu Glu Leu Lys Asp Asn Phe Lys Leu Met Cys Thr Asn Ala Met
260 195 200 205
263 Ile Tyr Asn Lys Pro Glu Thr Ile Tyr Tyr Lys Ala Ala Lys Lys Leu
264 210 215 220
267 Leu His Ser Gly Met Lys Ile Leu Ser Gln Glu Arg Ile Gln Ser Leu
268 225 230 235 240
271 Lys Gln Ser Ile Asp Phe Met Ala Asp Leu Gln Lys Thr Arg Lys Gln
272 245 250 255
275 Lys Asp Gly Thr Asp Thr Ser Gln Ser Gly Glu Asp Gly Gly Cys Trp
276 260 265 270
279 Gln Arg Glu Arg Glu Asp Ser Gly Asp Ala Glu Ala His Ala Phe Lys
280 275 280 285
283 Ser Pro Ser Lys Glu Asn Lys Lys Lys Asp Lys Asp Met Leu Glu Asp
284 290 295 300
287 Lys Phe Lys Ser Asn Asn Leu Glu Arg Glu Gln Glu Gln Leu Asp Arg
288 305 310 315 320
291 Ile Val Lys Glu Ser Gly Gly Lys Leu Thr Arg Arg Leu Val Asn Ser
292 325 330 335

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295 Gln Cys Glu Phe Glu Arg Arg Lys Pro Asp Gly Thr Thr Thr Leu Gly
296          340          345          350
299 Leu Leu His Pro Val Asp Pro Ile Val Gly Glu Pro Gly Tyr Cys Leu
300          355          360          365
303 Val Arg Leu Gly Met Thr Thr Gly Arg Leu Gln Ser Gly Val Asn Thr
304          370          375          380
307 Leu Gln Gly Phe Lys Glu Asp Lys Arg Asn Lys Val Thr Pro Val Leu
308 385          390          395          400
311 Tyr Leu Asn Tyr Gly Pro Tyr Ser Ser Tyr Ala Pro His Tyr Asp Ser
312          405          410          415
315 Thr Phe Ala Asn Ile Ser Lys Asp Asp Ser Asp Leu Ile Tyr Ser Thr
316          420          425          430
319 Tyr Gly Glu Asp Ser Asp Leu Pro Ser Asp Phe Ser Ile His Glu Phe
320          435          440          445
323 Leu Ala Thr Cys Gln Asp Tyr Pro Tyr Val Met Ala Asp Ser Leu Leu
324          450          455          460
327 Asp Val Leu Thr Lys Gly Gly His Ser Arg Thr Leu Gln Glu Met Glu
328 465          470          475          480
331 Met Ser Leu Pro Glu Asp Glu Gly His Thr Arg Thr Leu Asp Thr Gly
332          485          490          495
335 Lys Glu Met Glu Gln Ile Thr Glu Val Glu Pro Pro Gly Arg Leu Asp
336          500          505          510
339 Ser Ser Thr Gln Asp Arg Leu Ile Ala Leu Lys Ala Val Thr Asn Phe
340          515          520          525
343 Gly Val Pro Val Glu Val Phe Asp Ser Glu Glu Ala Glu Ile Phe Gln
344          530          535          540
347 Lys Lys Leu Asp Glu Thr Thr Arg Leu Leu Arg Glu Leu Gln Glu Ala
348 545          550          555          560
351 Gln Asn Glu Arg Leu Ser Thr Arg Pro Pro Gly Asn Met Ile Cys Leu
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356          580          585
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360 <211> LENGTH: 27
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362 <213> ORGANISM: Artificial Sequence
364 <220> FEATURE:
365 <223> OTHER INFORMATION: PI3 Kinase associated protein (PIKAP)
367 <400> SEQUENCE: 3
368 ccggggatcc ccatggctag ccatatg

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VERIFICATION SUMMARY

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